

SEQUENCE LISTING

<110> HEINZ, ERNST
 GIRKE, THOMAS
 SCHEFFLER, JODI
 SILVA, OSWALDO DA COSTA E

<120> PLANTS EXPRESSING DELTA-6-DESATURASE GENES,
 PUFAS-CONTAINING OILS FROM THESE PLANTS, AND A PROCESS
 FOR THE PREPARATION OF UNSATURATED FATTY ACIDS

<130> 0093/000032

<140> 10/019,048

<141> 2001-12-27

<150> DE 10030976.3

<151> 2000-06-03

<150> 09/347,531

<151> 1999-07-06

<160> 13

<170> PatentIn Ver. 3.3

<210> 1

<211> 2012

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (319)..(1896)

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tacctccggg ttttgagcg ggcaactct gttgcggctc ggaaggctat aggttcggca 180

ggagactgtt gattttatgt cgggggcatt gccattgtgg agagcggggg agactcagga 240

tctgtgagtg tgcgtgcagc gccccgactg ccgcagagcg tctgtgtatg acgaggttgt 300

tgtggagcgg cttttgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly

1

5

10

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Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu

15

20

25

ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc 447

Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser

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35

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gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt	495
Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val	
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tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat	543
Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn	
60 65 70 75	
tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag	591
Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys	
80 85 90	
ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta	639
Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu	
95 100 105	
tca gaa gta gca gta cac aac aag cca agc gat tgc tgg att gtt gta	687
Ser Glu Val Ala Val His Asn Lys Pro Ser Asp Cys Trp Ile Val Val	
110 115 120	
aaa aac aag gtg tat gat gtt tcc aat ttt gcg gac gag cat ccc gga	735
Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly	
125 130 135	
gga tca gtt att agt act tat ttt gga cga gac ggc aca gat gtt ttc	783
Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe	
140 145 150 155	
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Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr	
160 165 170	
att ggt gac gtg gag agg gtg gag ccg act cca gag ctg ctg aaa gat	879
Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp	
175 180 185	
ttc cga gaa atg aga gct ctt ttc ctg agg gag caa ctt ttc aaa agt	927
Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser	
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Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe	
205 210 215	
gct gcg agc att gca ata ata tgt tgg agc aag act att tca gcg gtt	1023
Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val	
220 225 230 235	
ttg gct tca gct tgt atg atg gct ctg tgt ttc caa cag tgc gga tgg	1071
Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp	
240 245 250	
cta tcc cat gat ttt ctc cac aat cag gtg ttt gag aca cgc tgg ctt	1119
Leu Ser His Asp Phe Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu	
255 260 265	

aat gaa gtt gtc ggg tat gtg atc ggc aac gcc gtt ctg ggg ttt agt	1167
Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser	
270 275 280	
aca ggg tgg tgg aag gag aag cat aac ctt cat cat gct gct cca aat	1215
Thr Gly Trp Trp Lys Glu Lys His Asn Leu His His Ala Ala Pro Asn	
285 290 295	
gaa tgc gat cag act tac caa cca att gat gaa gat att gat act ctc	1263
Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu	
300 305 310 315	
ccc ctc att gcc tgg agc aag gac ata ctg gcc aca gtt gag aat aag	1311
Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys	
320 325 330	
aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg	1359
Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu	
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Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr	
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Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu	
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Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser	
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Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu	
415 420 425	
gtt tat aat tgc tct aaa gaa ttc gtg agt gca cag atc gta tcc aca	1647
Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr	
430 435 440	
cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt	1695
Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu	
445 450 455	
aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat	1743
Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn	
460 465 470 475	
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Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly	
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 495 500 505

aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc 1887
 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr
 510 515 520

acc agt taa cagtctttgg aaagcttggc aattgatctt tattctccac 1936
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 35 40 45
 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
 50 55 60
 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
 65 70 75 80
 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
 85 90 95
 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
 100 105 110
 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
 115 120 125
 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
 130 135 140
 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
 145 150 155 160
 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
 165 170 175
 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
 195 200 205
 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
 210 215 220
 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
 225 230 235 240
 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
 245 250 255
 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
 260 265 270
 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
 275 280 285
 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
 290 295 300
 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
 305 310 315 320
 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
 325 330 335
 Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
 340 345 350
 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
 355 360 365
 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
 370 375 380
 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
 385 390 395 400
 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
 405 410 415
 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
 420 425 430
 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
 435 440 445
 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
 450 455 460
 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
 465 470 475 480
 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
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<212> DNA

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Lys Asp Glu Leu

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